

Db 240 IILNFFSFLYDWILFWCSCGSPFENIEKALSRVGTIVLCFLTLTYTGINMFCWSAVQ 299
QY 332 LRLADRLVDKQNGWGMGLHYSVRLVENVMVLKFGVKVLLNAYCHSLIALQLIAY 391
Db 300 LKIDSPLDKSHNWYQVLLVYVIRFENAILLWYLFKTYDYMVVCAPLLVLQLLIGY 359
QY 392 LISIDFMLLFFQYLHPLRSILTHNVVD-----YLHCVC--CHQ 427
Db 360 CTAILLPMLVYQFFHCKKLFSSSVSEGFQWLRRCFCWACRQ 401
RESULT 2
T32470
hypothetical protein F08F1.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
R:Accession: T32470
R:Fulton, B.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of *C. elegans* cosmid F08F1.
A:Reference number: Z11174
A:Accession: T32470
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-439 <FUL>
A:Cross-references: EMBL:AF026213; PIDN:AAB71305.1; GSPDB:GN00028; CESP:F08F1.5
A:Experimental source: strain Bristol N2; clone F08F1
C:Genetics:
A:Map position: X
A:Introns: 20/1; 72/3; 137/3; 184/2; 263/3; 289/3; 339/3; 369/1
C:Superfamily: *Caenorhabditis elegans* hypothetical protein F08F1.5
Query Match 5.6%; Score 129; DB 2; Length 439;
Best Local Similarity 19.4%; Pred. No. 0.004;
Matches 67; Conservative 62; Mismatches 98; Indels 118; Gaps 15;
QY 97 PLSLFWHLIL--LGPVIRCLEAMIKYLTWKKEQEPEYVSLTRKMLDGEVLEWEV 154
Db 126 PLSRMIVLCICQWGLPFWYKALY-YGMWPKSSNEN-----TDGEX----- 166
QY 155 GHSIRTLAMHRNAYKMSQ-----IQAFGLSVFOL----- 184
Db 167 -----RKCFKSWVERDATHLRFPEAFLESAPQLIOGSIAASYFQNYQTGY 216
QY 185 TYQYVSLISAEPVLRVLMVFLSVYTGATLCNNLAIQIKYDDYKIRGLPLEVLCIT 244
Db 217 PYWLYFOAAS-----LLLSIISISWVQNRSLMR--DDKVNWPHEAVLQF 264
QY 245 IWTLEITRLLILVLSATLKLKAVPFLVNLFLIILFEPWIKFWRSGAQMNNIEKNFS 304
Db 265 CWRFLTLARIITLVA-----LVLI-----GINVAIHIDA-CT 297
QY 305 RVGLTVLLSVTILYAGINFCWSALQRLADRLDVKQNGWGMGLHYSVRLVENVMV 364
Db 298 HIEKLLILN-ITFIHFIP-----NMVGNTRWRYL-TAYSVEFIE---MM 399
QY 365 LVKFFKGVKVLNCHSLIALQIILAYLISIDFMLLFFQYLHPLR 409
Db 340 LVCWLLPLSLNTPFYIEKVKVQGVPISPIAGIAMMYVYQFFHPNR 384
RESULT 3
E75203
hypothetical protein PAB2250 - *Pyrococcus abyssi* (strain Oresay)
C:Species: *Pyrococcus abyssi*
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
R:Accession: E75203
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: E75203

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <KAW>
A:Cross-references: GB:AJ248283; GB:AL096836; NID:G5457433; PIDN:CAR49076.1; PID:e15149
A:Experimental source: strain Oresay
C:Genetics:
A:Gene: PAB2250
Query Match 5.2%; Score 120.5; DB 2; Length 382;
Best Local Similarity 22.7%; Pred. No. 0.018;
Matches 83; Conservative 56; Mismatches 151; Indels 75; Gaps 14;
QY 72 SFEM---FSSIMVQLTLIFVHRDLAKDKPLSLFMHLIILGPIRCLEAMIKYLTWKKEE 128
Db 49 SFILARAFSSLSFGLL-----LEKDK-----RLIYLGSVTMAGNALIVHL----- 88
QY 129 QEBPYVSLTRKMLDGEVLE-----IEWEVGHSIRTLAMHRNAYKMSQIQAFGLSVP 182
Db 89 -----YPLTTSTWIOVVGIKILNGLNGISWPISQAFIASASPDNVRARVTSVYFFLASVA 143
QY 183 QLTYYQLYVSLISAEPVLRVLMVFLSVYTGATLCNNLA---IQIKYDDYKIRGLPLE 239
Db 144 SVIGN-YVYAQMAELTLKQMM---VASIFYLLTALSMPFLAYYLLFNYPVTPKRKGNVE 198
QY 240 VLCITWRTLEITSRLLIILVLFSA-----TLKLVKAVPFLVNLFLIIL 281
Db 199 ELHLDPRKVLVITSLIATITAFASGEITYVYVSEALGLGKGTAKLIGTGTATATL--- 255
QY 282 FEPWIKFWRSGAQMNNIEKNFSRVGTLLVVIS-----VTILYAGINFCWSALQRL- 335
Db 256 ---SYVTSWADYGVKREVMYSLLSMLASLSPLASIKTPTIV-FLGIFLALFSQAQSPRIS 312
QY 336 DRDLVDKQNGWGMGLHYSVRLVENVMVLFKFGVKVLLNCHSLIALQIILAYLISI 395
Db 313 RKVLVAYRRSSLAIG---GINAVQNVSTFLGGLFFGLAYSLGELSHLITVNLGLASFLPF 369
QY 396 DFMLL 400
Db 370 STALI 374
RESULT 4
T02024
cytochrome b245 beta chain homolog rbohA - rice (fragment)
N:Alternate names: intrinsic plasma membrane protein RbohAosp
C:Species: *Oryza sativa* (rice)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 23-Jul-1999
R:Accession: T02024
R:Keller, T.; Damude, H.G.; Werner, D.; Doerner, P.; Dixon, R.A.; Lamb, C.
submitted to the EMBL Data Library, July 1997
A:Description: A plant homolog of the neutrophil NADPH oxidase gp91phox subunit gene en
A:Reference number: Z14499
A:Accession: T02024
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-745 <REL>
A:Cross-references: EMBL:AF015302; NID:G2654869; PID:G2654870
C:Genetics:
A:Gene: rbohA
C:Keywords: calcium binding; membrane protein
Query Match 5.2%; Score 119.5; DB 2; Length 745;
Best Local Similarity 20.7%; Pred. No. 0.047;
Matches 89; Conservative 66; Mismatches 171; Indels 103; Gaps 18;
QY 40 STFLYC-GEAASALYVRIYKNSYRMTY-TFSFPMFSSIMVQLTLIFVHRDLAKDKP 97
Db 11 SFAECIGTWTESEFALELFTLSRRRQMKVDITNDELREINQOIT-----DNSFDSR 64
QY 98 LSLFMHLIILGPIRCLEAMIKYL-----TLWKKEQEPEYVSLTRKMLDGEVLE 149
Db 65 LQIFFEVDKNDAGRITAEVKEIIMLSASANKLSRLKEQAEYAAALIMEELDPGLGYI 124

QY 150 IEWEVGHSTIRTLAMHNRNAYKRMQI-----QAPLGSVPOLTYQLYVSLISAEPVLRVVL 204
 Db 125 ELWQ-----LETLLOKDTYNTSYQALSYTSQALSKAGLRKKSKIRKS----- 170
 QY 205 MVFSLVSVTYGATLNCNMLAIQIKYDDYKIRLGPVLCIT-----WRTLEITSRLIL 258
 Db 171 -----TSLSY-----YFEDNWKRLWVL-ALWIGIMAGLFTWPKMQYRNRYFED 212
 QY 259 VL-FSATLKLKAVPPLVNLFLILPE-----PWIKFWSGAQMPNNIEKFSRVGTLLV 311
 Db 213 VMGVCVTTAKGAETLKNMAIILLPVCTITWLRSTRAARALPFDNNINPHKTTAAAI 272
 QY 312 LISVILYAGINFSWSALQRLADRLVDKQNGHMGMLHY-----SVRLVENVMVLV 366
 Db 273 VVGI-ILHAGNLVCDPRLIKSSDEKYPALGQYFGEIKPTFTLVKVGEGITGVIMVC 331
 QY 367 F-----KFFGVKLLNYCHSL-----IALQLII-----AYLISD 396
 Db 332 MIAFTLATRWRFRSLVKLPRPDKLTGFNAFW-YGHHLFIIVYIALIVHGECLYLIHW 390
 QY 397 FMLLFFOYL 405
 Db 391 YRRTTWML 399

RESULT 5
 A:Accession: A96825
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-783 <STO>
 A:Cross-references: GB:AE005173; NID:g4835769; PIDN:AAD30236.1; GSPDB:GNO0141
 A:Gene: T8K14.18
 A:Map position: 1

hypochemical protein T8K14.18 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: A96825
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hultzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A96825
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-783 <STO>
 A:Cross-references: GB:AE005173; NID:g4835769; PIDN:AAD30236.1; GSPDB:GNO0141
 A:Gene: T8K14.18
 A:Map position: 1

Query Match 5.1%; Score 118.5; DB 2; Length 783;
 Best Local Similarity 19.6%; Pred. No. 0.06;
 Matches 89; Conservative 69; Mismatches 166; Indels 129; Gaps 19;

QY 73 FMFSSIMVQLTILFVHRDL-----AKDKPLSLFMHLILGPVIRCLEAMIKYLTW 124
 Db 16 FPLNTMTFQMACILVFSOLFVLLRLPCGQAGVAQIAGIVLSPLLRIPKVKRFFLQ 75
 QY 125 KKEQEPEPVVS--LTRKKMLIDGEEVLEWEVGHSTIRTLAMHNRNAYKRMQI--QAFL-- 178
 Db 76 KVAADYISFFSALRTSFMLGLEVDLHF-----MRN-FKAAVITLSGFVVS 124
 QY 179 GSVPOLTYQLYVSLISAEPVLRVLMVFSVSVTYGATLNCNMLAIQIKYDDYKI---RL 235
 Db 125 GLLSFASLMFLPLFGIKEDYFTFFLVLLVLTSLNTASPVVRSIA-----DWKLTNCEI 178
 QY 236 GPVLCITITWRTLETSRLILVLFSATLKLKAVPPLVNLFLILPE-----PWIKFWS 291
 Db 179 GLRITSCALFIELTNVLYTIINAFISGTTILEFLFLATVALILINMVLAPWL----- 233
 QY 292 GAQMPNNIEKFSRVGTLLVLI-----SVTILYAGINFSWSALQRLA 335

Db 234 --PKXNPKEKYLKSAETLVFFIFLLIIGITIBSYDYNSSVSFAIGIMFP-----ROGKT 286
 QY 336 DRDLVDK-----GQNGHMGMLHYSV-----RLVENVMVLVFKFPGV----- 372
 Db 287 HRTLQRLSYPIHEFVLPVYFGVIGFRFSIIALTKEFYLGIIVIVITVITAGKIGVISAC 346
 QY 373 -----KVLL--NY-----CHSLIALQLIIAYLIS--- 394
 Db 347 MYLKIPKPYWLFPLTILSVKGVHGLLLDSNYSEKKWTTTIHDMVVAALVITLVSGVL 406
 QY 395 IDFMLLFFQ--YLHLRLSLFTNNVDYLHCVC 425
 Db 407 ASFLKTRKDFAYEKTSLSHNTNEELRLSC 439

RESULT 6
 D90567
 hypochemical protein MYP 4440 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C:Species: Mycoplasma pulmonis
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
 C:Accession: D90567
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
 Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
 A:Reference number: A99512; MUID:21267165; PMID:11353084
 A:Accession: D90567
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-508 <KUR>
 A:Cross-references: GB:AL445566; PID:g14089850; PIDN:CAC13617.1; GSPDB:GNO0153
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYP 4440
 A:Genetic code: SGC3

Query Match 4.9%; Score 113.5; DB 2; Length 508;
 Best Local Similarity 18.3%; Pred. No. 0.096;
 Matches 81; Conservative 90; Mismatches 159; Indels 113; Gaps 20;

QY 28 NRPFFPFSILSTFLYCEASALYMWIRYKN-----SETYRMTYTFSP---FMFS 77
 Db 95 NHRNFYIILWFSIYIFSG-----IFILFSRNIPNFIPTNEFVELGYFYFYVYVIFL 147
 QY 78 SJMVQLTLFVHRDLAKDKPLSLFMHLILGPVIRCLEAMIKYLTWKKBEQEPYVSLT 137
 Db 148 EILYSVYLLYNRRVRDHLKYLKIVL--IVSMYVLI--FSSWINKSQ-----IT 197
 QY 138 RKMLID-----GEEV--LIEWEVGHSTIRTLAMHNRNAYKRMQIQAFL 178
 Db 198 TDAKLVEWLPFQNRIOAFVEASDEIVGLIFREIGYVIAVLIL--IPFFPSLLYS 254
 QY 179 GSVPOLT-----YQLYVSLISAEPVLRVLMVFSVSVTYGATLNCNMLAIQIKYD 229
 Db 255 FKPKRTRKVSQKKNLQFNLSIIVLISITFLNYWIIIFKNVVSF-----LEIN 303
 QY 230 DYKIRLGPVLCIT---IWRLEITSRLILVLFSATLKLKAVPPLVNLFL--LILFEPW 285
 Db 304 NULGLNVVFLVFTFELILNRLKSS--IYPMFSVSP-----FIVSFFFTLIIFH-- 353
 QY 286 IKFWRSGAQMNNIEKFSRVGTLLVLIISVTILYAGINFSWSALQRLADRLVDKQON 345
 Db 354 ISYDR-----ENKISMFNILLIFSFTVILFIFLFSNYEMSTLOKMSFNL----- 398
 QY 346 WGHMGMLHYSVRLVENVMVLVFKFPGVKKVLLNYCHSLIALQLIIAYLISIDFMLLFFOYL 405
 Db 399 -----LLTSFSL--YIFMSVIHKDLLVITIANFLDFYLLLYLVGFAVMLNFFVVFVSFY 452
 QY 406 HPLRSLFTH-----NVVDY 419
 Db 453 KSLSTLTKTEKPKWTFNKNIFDY 475

RESULT 7

A86299
hypothetical protein F309.18 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
R:Accession: A86299
R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mailli, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86299
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-785 <STO>
A:Cross-references: GB:AE005172; NID:g4966359; PIDN:AAD34690.1; GSPDB.GN00141
C:Genetics:
A:Map position: 1

Query Match 4.9%; Score 112.5; DB 2; Length 785;
Best Local Similarity 19.7%; Pred. No. 0.19;
Matches 89; Conservative 84; Mismatches 172; Indels 107; Gaps 20;

QY 37 ILFSTFLY-----CGAAS-----ALVMYRIYKNSYRTMTYTFSPFSSIMVOL 83
Db 30 LVFSQFYFLFKPCGQGPVQAQILAGIVLSLLTIIRKVEFFLQKDSASYIYFFSLRT 89
QY 84 TLIF-VHRDLAKDKPLSFMHLLILGVPVIRCLAMIKYLTWKKEQEPYVSLTRKML 142
Db 90 AFVFLIGLEIDL-----PMKRNKNSIVITLGLSVITSGIWL-----PFLWFLIRFMQ 138
QY 143 IDGE-----EVLIEWEVS-----IRTLAMHRYKMSQIOAFLGS 180
Db 139 IKGDFLTFYLAFLITSNTPVIRSIIIDKLTSEIGRLAISGLFIBITWI----- 192
QY 181 VPQTYQLYVSLISAEVPLGRVVLVPLSVSVTYGATLCNMLAIQIKYDDYKIRLGPLE- 239
Db 193 ---PIYIVLSPISGTMTADIFYSPATGVIIILNRLASMLPKRNPKYLSKAETLAF 249
QY 240 -VLCITITWTL---ITSRLLIU---LFSATLK-----LKAVPFLVNLPLIILFPWK 287
Db 250 IILILIALTIESNLNLTFLVPIIGLMPREGKTVRTLQRLSYPIHEPVLVPYFGYIG 309
QY 288 FWRSGAQMNNIEKNSRVGTLVVLISVTILYAGINPSC-----WSALQLRLADRD 338
Db 310 FRPS-----VNSLTRHYLVLGMTVALSLGKLGVLVLFACFLPKQYWLFLSTLMSVK- 364
QY 339 LVDKGQWGMHGLHYSVRLVENVIMVLVFKFFGVKLLNCHSLIALQLIAYLIS--ID 396
Db 365 -----GHIGL-----VLDSN-----LMYKKWTPPV-----HDMFVAALVIMTLSSVIT 405
QY 397 FMLLFFQ-----YLHPLRSFLTHNVVDVHLVCC 425
Db 406 SLLRSQKSFSAHIKTSLELFDTEELRLVLT 437

RESULT 8
B97305
probable cation efflux pump (multidrug resistance protein) [imported] - Clostridium ace
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
R:Accession: B97305
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97305

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-461 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK81229.1; PID:g15026374; GSPDB.GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3295

Query Match 4.7%; Score 109.5; DB 2; Length 461;
Best Local Similarity 20.5%; Pred. No. 0.19;
Matches 91; Conservative 79; Mismatches 145; Indels 129; Gaps 24;

QY 33 FPF-SILFSTFLYCGAASALYVRIY-RKNSETYR-----MTYTFSEFMF 76
Db 58 FPIQKLIANGLLIATGAST-YAARVIGEKYKELKIVINSALTIVSISIFLQF 116
QY 77 -SSIMVQLTILFVHRDLAKDK--PLSL-FMHLILGVPVIRCLAMIKYLTWKKEQEEP 132
Db 117 KSSILYSLG-----ASDNTYPMAVQYISIIIFGSIIFMCLASVMSYI----- 157
QY 133 YVSLTRKMLIDGE-----EVLIEWEVS-----GHSIRTLAMHRYKMSQIOAF 177
Db 158 MVSGLGKTKLLTYNIVGVLLNIILNVLVIQLHMGIRGSGIATV-----LSQLAAF 208
QY 178 LGSVPOLTY-----QLVSLISAEVPLGRVVLVPLSVSVTYGATLCNMLAIQI 226
Db 209 VVALVGFAYNKKQNFENISTNIISGDI-IREIVLVGFSTFIIIEIADAVSGLNVV 267
QY 227 KY----DDYKIRLGPLEVCITWRT-LEITSRLILVLFS-----ATLKLA 269
Db 268 LYAGGDSALIMLGVTIKVMFMFIVIGISSGMQPIGVNFGAGNYKAKDKILKFSKT 327
QY 270 V-----PFLVNLFLIILFEPWIKFWRSGAQMNNIEKNSRVGTLVVLISVTILYAGINFS 325
Db 328 VIIISAFVWVG-F-IIWAQPLIGFLKDAQLVSKTVSAFRIVISMLPLG--IYVVAIYY 384
QY 326 CWSALQLRLADRLVDKQWGMHGLHYSVRLVENVIM-----VLVFKFFGVK-VLLNYC 379
Db 385 -----QAIGEARISFILSIYRELIMFIPMAVILFKIVGINGVFIAY- 425
QY 380 HSLIALQLIAYLISIDFMLLFFQ 403
Db 426 ----PLTDIIVILTSYVYFIRRAFK 445

RESULT 9
T11039
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Chlamydomonas eugametos mitochol
C:Species: mitochondrion Chlamydomonas eugametos
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T11039
R:Denovan-Wright, E.M.; Nedelcu, A.M.; Lee, R.W.
Plant Mol. Biol. 36, 285-295, 1998
A>Title: Complete sequence of the mitochondrial DNA of Chlamydomonas eugametos.
A:Reference number: Z17244; MUID:98145434; PMID:9484440
A:Accession: T11039
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-498 <DEN>
A:Cross-references: EMBL:AF008237; NID:g2865253; PID:g2865257; PIDN:AAC39340.1
C:Genetics:
A:Genome: mitochondrion
A:Note: nad4
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 4.7%; Score 109.5; DB 2; Length 498;
Best Local Similarity 22.1%; Pred. No. 0.2;
Matches 64; Conservative 46; Mismatches 89; Indels 91; Gaps 13;

QY 185 TYQLYVSLISAEVPLGRVVLVPLSVSVTYGA-----TLCNMLAIQIKYDDYKIRL- 235
Db 40 TYCLFTVMV-----VLLNTLYLWSI-YDAIGHSLQWVVIIRLHISFGVDSMSLSLT 90

C:\Date: 19-May-2000 #sequence revision 19-May-2000 #text change 03-Jun-2002

[illegible]

RESULT 10
Tl7163
NADH2 dehydrogenase (ubiquinone) [EC 1.6.5.3] chain 4 [similarity] - Pygathrix bieti mitochondrion Pygathrix bieti
C/Species: Mitochondrion Pygathrix bieti
C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002
C/Accession: Tl7163
R/Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; Xie, J.; Primatol. 18, 305-320, 1997
A/Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences
A/Reference number: 218709

Query Match	4.7%	Score 108;	DB 2;	Length 459;
Best Local Similarity	19.2%	Pred. No. 0.25;		
Matches 80;	Conservative 71;	Mismatches 143;	Indels 122;	Gaps 19;

Qy	35	PSILFSTFLYCGEAA	SLYVMVIRYKQ	SEYRMVYTSF	PMFSSIMVQLT	LIIVHRDLAK	94
Db	118	FYILFETTLPTLII	TRWGQAE	RLNASTFYLT	-----GSLPL	ILMLFVHN	173
Qy	95	DKPLSLFMHLL	GPVIRCL	EAMIKYLT	LWKKEQ	EEPPVSLTRKKML	154
Db	174	-----LNI	-----	PLITLTAOKI	-----	TTTTT	190

[illegible]

RESULT 11
T17166
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti mitochondrion
C:Species: mitochondrion Pygathrix bieti

C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002
C:Accession: T17166
R:Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; X:
Int. J. Primatol. 18, 305-320, 1997
A:Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences
A:Reference number: Z18709
A:Accession: T17166
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <WAN>
A:Cross-references: EMBL:U92957; NID:g2290441; PID:g2290444; PIDN:AAD08826.1
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match	4.6%	Score 107;	DB 2;	Length 459;
Best Local Similarity	19.2%;	Pred. No. 0.3;		
Matches 80: Conservative	71;	Mismatches 143;	Indels 122;	Gaps 19;

Qy	35	PSILPSTFLYCGEAAASALYVVRIRKUNSEYRMTYTSPFMPSSIMVOLTLIFVHRDLAK	94
Db	118	FYLIFETTLPTLIITRWGNQAEPLNASTFYLYTIT-----GSLPLLIIIMLLFVNHNIGS	177
Qy	95	DKPLSLFMHILLGPVIRCLEAMIKYLTLWKKEBEEBPYVSLTRKKMLIDGEEVLIEWEV	155
Db	174	--LNI-----PLLTIAQKL-----TTTW--	190
Qy	155	GHSRTTLAMHRNAYKRMSIQAFLGSPVQLTYQLYSLSISAEVPL-GRVVLMVFSLSVVT	213
Db	191	SHNLTWLAC-----MMAFVKNPKPLYCLHLWLPKAHVAPIAGSMVLAVALLKGG	246
Qy	214	YG----ATLCNMALAIQYDDYKIRGLPGLEVLCITIVRTLETISRLLIILVFSATLKKA	266
Db	241	YGMRLTSILNPLETEYMAY-----PFLMLSLGMGMTSTCTLRQTDLSLIAYS	299
Qy	270	VPFLVLNFLIILPE-PHIKWFRSGAQMNNIEKNFSRVGTLVLI-----SVTLIYAGI	322
Db	291	VSHMALVMASLIQTWP-----STGAIVLMIAHGLTSSMLFCUANS	333
Qy	323	NFSCWSALQRLDARDLVDK-----GQNWHMGMLHYSVRLV-ENVIMVLVFKPFVG	372
Db	333	NYERTHS-RIMLSRGLOTLPLMAFWFAANLTNALPPTINLI GELLVMMTSSFSSHV	391
Qy	373	KVLNLYCHSLIALQIIAYLISIDFMLLFFQ-----YLHPILRSFLT-HNVVDYLH	421
Db	392	TIMIT-----GLNMLITAYSL-YMLVTTQRETLTTHIINKMKSPTRENLMEMH	440

RESULT 12

T17172
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti mi
 C:Species: mitochondrion Pygathrix bieti
 C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002
 C:Accession: T17172
 R:Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; X
 Int. J. Primatol. 18, 305-320, 1997
 A:Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences
 A:Reference number: Z18709

A. Residues: 1-459 <WAN>
A. Cross-references: EMBL:U92959; NID:g2290449; PID:g2290452; PIDD:AAD08832.1
C. Superfamily: NADH dehydrogenase (ubiquinone) chain 4
D. Description: mitochondrial complex I microdomain.
E. Function: oxidative phosphorylation.

Query Match 4.6%; Score 107; DB 2; Length 459;
Best Local Similarity 19.2%; Pred. NO. 0.3;
Matches 80; Conservative 71; Mismatches 143; Indels 122; Gaps 19;

QY		35	FSILPSTFLYCGEAASALYMVRIYRKNSETYRMVTYTFSPFMFSSIMVOLTLIFVHRDLAK	94
		:	: : : : :	:
		:	: : : : :	:
		:	: : : : :	:
		:	: : : : :	:
D6		118	FYLPEFTLLIPTLIITRWGNQAERLNASTYFYFTLT-----GSEPLLMLLIVFHNNUGS	177

